**Amendments to the Specification:**

Please add the following new section on page 2 after line 23 as follows:

Brief Description of the Drawings

Figure 1 presents the amino acid sequence of Taq DNA polymerase (SEQ ID NO:1) isolated from the thermophilic bacterium *Thermus aquaticus*.

Figure 2 presents the amino acid sequence of a modified Taq DNA polymerase (SEQ ID NO:2).

Figure 3 presents the amino acid sequence of another modified Taq DNA polymerase (SEQ ID NO:3).

Figure 4 shows salt tolerance data for one of the modified Taq DNA polymerases (SEQ ID NO:2), as compared to that of a known modified Taq DNA polymerase (TS).

Figure 5 shows the thermostability of one of the modified Taq DNA polymerases (SEQ ID NO:2), as compared to a commercial Taq DNA polymerase (Amplitaq).

Figure 6 is an electropherogram of sequence reaction products (SEQ ID NO:6) generated using a commercial Taq DNA polymerase (Thermosequenase Version II, or TSII).

Figure 7 is an electropherogram of sequence reaction products (SEQ ID NO:7) generated using one of the modified Taq DNA polymerases (SEQ ID NO:2).

Figure 8 is an electropherogram of sequence reaction products (SEQ ID NO:8) of a difficult to sequence template. Reaction is performed using TSII.

Figure 9 is an electropherogram of sequence reaction products (SEQ ID NO:9) of a difficult to sequence template. Reaction is performed using the modified Taq DNA polymerase of SEQ ID NO:2.

Figure 10 shows a comparison of a portion of the sequence in Figure 6 (Figure 10a, SEQ ID NO:10) with the same portion of sequence in Figure 7 (Figure 10b, SEQ ID NO:10).

Figure 11 shows a comparison of two electropherograms of sequence reaction products (SEQ ID NO:11), generated using TSII (Figure 11a), or the modified Taq DNA polymerase of SEQ ID NO:2 (Figure 11b).

Figure 12 shows a comparison of two electropherograms of sequence reaction products (SEQ ID NO:12), generated using TSII (Figure 12a), or the modified Taq DNA polymerase of SEQ ID NO:2 (Figure 12b).

Figure 13 is a side-by-side comparison of electropherograms obtained from sequencing reactions conducted using D18A/F667Y Taq DNA polymerases having various E681 substitutions as described at the left of each electropherogram. From top to bottom: E681 (SEQ ID NO:13); E681H (SEQ ID NO:14); E681R (SEQ ID NO:15); E681M (SEQ ID NO:16) and E681W (SEQ ID NO:16).

Figure 14 shows the relative reactivity compared to unlabelled ddNTPs evidenced in four color sequencing reactions which employed D18A/F667Y and various E681 substitutions thereof with various charged terminators.

Figure 15 depict structures with potential sites at which a charged moiety may be attached to the terminator.

Figure 16 shows electropherograms of sequencing reactions completed with either a normal energy transfer terminator (Figure 16a), or a Bis-sulfonated fluorescein ET terminator (Figure 16b).

Figure 17 shows electropherograms of sequencing reactions completed with dye labeled dideoxynucleotides containing various net negative charges. Figure 17a: FAM-11-ddCTP. Figure 17b: Compound 7. Figure 17c: Compound 8.

Figure 18 shows an electropherogram of a sequencing reaction using a terminator with a net negative charge of three (compound 10). Reaction mixture was directly loaded with no clean-up procedure, demonstrating the utility of negatively charged terminators with respect to direct load sequencing.

Figure 19 shows electropherograms of sequencing reactions completed with a net +2 charge terminator (compound 27), with (Figure 19b) or without (Figure 19a) phosphatase treatment prior to loading.

Please replace the paragraph on page 7, lines 11-19, with the following amended paragraph:

The new E to R amino acid modification discovered also results in increased uniformity in termination events during sequencing reactions containing net positive, negative, or neutrally charged dideoxynucleotide terminators. This results in an increased uniformity in electropherogram band intensity and an increase in the number of bases which can be ~~basedcalled~~ basecalled per sequence. For example, as shown in Figure 6, the average deviation of band intensity using Thermosequenase

Version II is about a 30% deviation. However, as shown in Figure 7, a typical result using an E to R polymerase is about a 22% deviation. This improvement is significant. Portions of Figures 6 and 7 are magnified in Figure 10 ~~Figures 8 through 10~~ for comparison purposes.

Please replace the paragraph on page 8, lines 27-29, with the following amended paragraph:

Figure 14 shows the relative reactivity compared to unlabelled ddNTPs evidenced in four color sequencing reactions which employed D18A/F667Y and various E681 substitutions ~~therEof~~ thereof with various charged terminators.

At the end of the written description, before the claims, please delete the previously submitted "Sequence Listing" and insert the revised "Sequence Listing" attached hereto.